

Sequence Listing

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 ZF0050330= Bacillus; ZF0051303= Bacterium; ZF0051337=
 Methylobacter; ZF0051321= Bacterium; ZF0050782= Lactobacillus
 30 bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=
 Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=
 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0002031=
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
 Streptomyces; ZF0002437= Streptomyces; ZF0003712=
 35 Micromonospora; ZF0003765= Streptomyces; ZF0051305= Bacterium;
 ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018=
 Streptomyces; ZF0003767= Actinomyces; ZF0002332= Streptomyces
 diastatochromogenes; ZF0003768= Actinomyces; ZF0002379=
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 115 120 125
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 Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=
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35 40 45

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20 Thr Asp Ala Gly Leu Thr Pro Tyr His Ala Ile Lys Arg Ser Leu Pro
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Lys Leu Arg Gly Gly Ser Tyr Ala Val Val Ile Gly Thr Gly Gly Leu
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35 40 45

His Leu Val Pro Ile Gly Asp Leu Asp Pro Val Thr Thr Val Pro Leu
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5 Thr Asp Ala Gly Leu Thr Pro Tyr His Ala Ile Lys Arg Ser Leu Gly
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10 Lys Leu Arg Ala Gly Ser Tyr Ala Val Val Ile Gly Thr Gly Gly Leu
 85 90 95

15 Gly His Val Gly Ile Gln Leu Leu Arg His Leu Ser Pro Ala Arg Ile
 100 105 110

20 Ile Ala Leu Asp Val Asn Asp Glu Lys Leu Ala Phe Ala Arg Glu Val
 115 120 125

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25	ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=		
	Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes		
	nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=		
	Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;		
	ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=		
30	Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;		
	ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;		
	ZF0003528= Actinomyces; ZF0003529= Actinomyces;		
	<400> 16		
35	Gly Leu Thr Ile Gly His Glu Pro Val Gly Val Ile Glu Lys Leu Gly		
	1 5 10 15		
40	Ser Ala Val Thr Gly Tyr Arg Glu Gly Gln Arg Val Ile Ala Gly Ala		
	20 25 30		
45	Ile Cys Pro Asn Phe Asn Ser Tyr Ala Ala Gln Asp Gly Ala Pro Ser		
	35 40 45		
50	Gln Asp Gly Ser Tyr Leu Val Ala Ser Gly Ala Cys Gly Cys His Gly		
	50 55 60		
55	Tyr Arg Ala Thr Ala Gly Trp Arg Phe Gly Asn Ile Ile Asp Gly Ala		
	65 70 75 80		
	Gln Ala Glu Tyr Leu Leu Val Pro Asp Ala Gln Gly Asn Leu Ala Pro		
	85 90 95		

Val Pro Asp Asn Leu Ser Asp Glu Gln Val Leu Met Cys Pro Asp Ile
 100 105 110

5 Met Ser Thr Gly Phe Lys Gly Ala Glu Asn Ala His Ile Arg Ile Gly
 115 120 125

10 Asp Thr Val Ala Val Phe Ala Gln Gly Pro
 130 135

<210> 17

15 <211> 144

<212> PRT

20 <213> unknown

<220>

<221> source

25 <223> ZF0050197= Pseudomonas oleovorans; ZF0050294= Rhodococcus;
 ZF0050330= Bacillus, ZF0002852= Rhodococcus; ZF0050310=
 Arthrobacter paraffineus; ZF0002437= Streptomyces; ZF0003712=
 Micromonospora; ZF0003765= Streptomyces; ZF0002332=
 Streptomyces diatsatochromogenes; ZF0003768= Actinomyces;
 30 ZF0002379= Streptomyces coelestis; ZF0002443= Streptomyces;
 ZF0002442= Streptomyces; ZF0002436= Streptomyces; ZF0050994=
 Bacterium; ZF0050992= Bacterium; ZF0050442= Bacterium;
 ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=
 Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes
 35 nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=
 Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;
 ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=
 Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;
 ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;
 40 ZF0003528= Actinomyces; ZF0003529= Actinomyces;

<400> 17

Cys Gly Thr Asp Leu His Ile Leu Gly Gly Asp Val Pro Glu Val Thr
 45 1 5 10 15

Asp Gly Arg Ile Leu Gly His Glu Ala Val Gly Thr Val Val Glu Val
 20 25 30

50 Gly Asp Gly Val Gln Thr Leu Ala Pro Gly Asp Arg Val Leu Val Ser
 35 40 45

55 Cys Val Thr Ala Cys Gly Thr Cys Arg Phe Cys Arg Glu Ser Arg Tyr
 50 55 60

Gly Gln Cys Leu Gly Gly Gly Gly Trp Ile Leu Gly His Leu Ile Asp
 65 70 75 80

5 Gly Thr Gln Ala Glu Leu Val Arg Val Pro Tyr Ala Asp Asn Ser Thr
 85 90 95

10 His Arg Ile Pro Asp Gly Val Ser Asp Glu Gln Met Leu Met Leu Ala
 100 105 110

15 Asp Ile Leu Pro Thr Ser Tyr Glu Val Gly Val Leu Asn Gly Cys Leu
 115 120 125

20 Arg Pro Ala Asp Val Val Val Ile Ile Gly Ala Asp Asp Arg Pro Leu
 130 135 140

<210> 18

25 <211> 73
 <212> PRT
 <213> unknown

30 <220>
 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*

35 <400> 18

Val Asp Val Val Val Asp Asn Ala Gly Phe Gly Thr His Gly Ala Phe
 1 5 10 15

40 Val Asp Glu Asp His Glu Arg Val Thr Ser Glu Ile Gln Leu Asn Ile
 20 25 30

45 Ala Thr Leu Val Glu Leu Thr His Thr Phe Pro Pro Asp Leu Leu Thr
 35 40 45

Gly Arg Gly Ala Leu Val Asn Ile Ala Ser Thr Ala Ser Phe Gln Pro
 50 55 60

5 Thr Pro Gly Met Ala Val Tyr Cys Ala
 65 70

10 <210> 19
 <211> 75
 <212> PRT

15 <213> unknown
 <220>

20 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 19

25 Val Asp Val Val Val His Asn Ala Gly Phe Gly Thr His Gly Ala Phe
 1 5 10 15

30 Val Asp Glu Asp Leu Glu Arg Val Thr Ser Glu Ile Gln Leu Asn Ile
 20 25 30

35 Ala Thr Leu Val Glu Leu Thr His Thr Phe Leu Pro Asp Leu Leu Thr
 35 40 45

40 Gly Arg Gly Ala Leu Val Asn Ile Ala Ser Thr Ala Ser Phe Gln Pro
 50 55 60

45 Thr Pro Gly Met Ala Val Tyr Cys Ala Thr Lys
 65 70 75

50 <210> 20
 <211> 79
 <212> PRT

55 <213> unknown
 <220>

<221> source
 <223> ZF0003535= *Actinomyces*
 <400> 20

Arg Val Asp Val Val Val His Asn Ala Ala Ile Thr Gln Lys Ala Thr

<212> PRT
<213> unknown
5 <220>
<221> source
<223> ZF0050310= *Arthrobacter paraffineus*
10 <400> 22
Gln Gly Ile Gly Tyr Ala Thr Ala Lys Arg Leu Ile Ser Leu Gly Ala
1 5 10 15
15 Thr Val Ala Ile Gly Asp Ile Asp Glu Ala Thr Leu Ala Arg Ala Ala
20 25 30
20 Lys Asp Leu Gly Ile Arg Thr Phe Gly Arg Leu Asp Val Thr Asp Pro
35 40 45
25 Ala Ser Phe Phe Asp Phe Leu Asp Thr Val Glu Gly Glu Leu Gly Pro
50 55 60
30 Ile Asp Val Leu Ile Asn Asn Ala
65 70
<210> 23
35 <211> 75
<212> PRT
<213> unknown
40 <220>
<221> source
<223> ZF0050310= *Arthrobacter paraffineus*
45 <400> 23
Gln Arg Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala
1 5 10 15
50 Thr Val Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val
20 25 30
55 Ala Glu Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val
35 40 45

Arg Asp Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala
 50 55 60

5 Phe Gly Pro Val Asp Val Met Met Asn Asn Ala
 65 70 75

10 <210> 24
 <211> 72
 <212> PRT

15 <213> unknown
 <220>
 <221> source
 20 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 24

25 Gln Gly Ile Gly Tyr Gln Thr Ala Lys Glu Leu Ile Arg Arg Gly His
 1 5 10 15

30 Arg Val Ala Ile Gly Asp Ile Asp Glu Ala Arg Ala Lys Glu Thr Ala
 20 25 30

35 Ala Glu Leu Gly Val Lys Val Val Thr Arg Leu Asp Val Thr Asp Pro
 35 40 45

40 Asp Ser Phe Lys Asp Phe Leu Asp Leu Val Glu Gly Asp Leu Gly Pro
 50 55 60

45 Leu Asp Val Leu Ile Asn Asn Ala
 65 70

50 <210> 25
 <211> 74
 <212> PRT
 <213> unknown
 <220>
 <221> source
 55 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 25

Gly Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala Thr
 1 5 10 15
 5 Val Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val Ala
 20 25 30
 10 Glu Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val Arg
 35 40 45
 Asp Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala Phe
 50 55 60
 15
 Gly Pro Val Asp Val Ile Val Asn Asn Ala
 65 70
 20
 <210> 26
 <211> 74
 25
 <212> PRT
 <213> unknown
 30
 <220>
 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 35
 <400> 26
 Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala Thr Val
 1 5 10 15
 40 Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val Gly Glu
 20 25 30
 45 Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val Arg Asp
 35 40 45
 50 Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala Phe Gly
 50 55 60
 55 Pro Val Asp Val Met Val Asn Asn Ala Gly
 65 70
 <210> 27
 <211> 62

<212> PRT
 <213> unknown
 5 <220>
 <221> source
 <223> ZF0002333= Rhodococcus erythropolis
 10 <400> 27
 Val Pro Val Ala Val Val Asp Leu His Ile Glu Ser Ala Lys Glu Thr
 1 5 10 15
 15
 Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala Leu Ala Leu Glu
 20 20 25 30
 Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala Phe Glu Ala Thr
 35 40 45
 25 Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn Asn Ala
 50 55 60
 30 <210> 28
 <211> 74
 <212> PRT
 35 <213> unknown
 <220>
 40 <221> source
 <223> ZF0002333= Rhodococcus erythropolis
 <400> 28
 45 Leu Gly Arg Glu Ile Ala Leu Lys Leu Ala Ser Glu Gly Ala Ser Val
 1 5 10 15
 Val Val Asn Asp Leu Asp Pro Glu Pro Ala Ala Gln Thr Glu Arg Asp
 50 20 25 30
 Ile Lys Ala Thr Gly Gly Gln Ala Val Ser Cys Val Gly Ser Val Ala
 55 35 40 45
 Glu Asp Gly Phe Ala Glu Arg Phe Val Asn Thr Ala Val Glu Ser Phe
 50 55 60

Gly Gly Leu Asp Val Met Val Asn Asn Ala
 65 70

5
 <210> 29
 <211> 76

10
 <212> PRT
 <213> unknown
 <220>

15
 <221> source
 <223> ZF0002333= Rhodococcus erythropolis
 <400> 29

20
 Ala Gly Leu Gly Val Glu Phe Ala His Arg Phe Ala Ala Arg Gly Ala
 1 5 10 15

25
 Asn Leu Val Leu Val Ala Arg Arg Ala Asp Arg Leu Glu Ala Leu Ala
 20 25 30

30
 Thr Glu Leu Arg Val Ala His Gly Ile Thr Val Thr Val Leu Pro Ala
 35 40 45

35
 Asp Leu Ala Ala Pro Gly Val Gly Ala Thr Leu His Gln Glu Leu Thr
 50 55 60

40
 Ser Arg Gly Ile Thr Val Thr Ser Leu Ile Asn Asn
 65 70 75

45
 <210> 30
 <211> 72
 <212> PRT
 <213> unknown
 <220>

50
 <221> source
 <223> ZF0003535= Actinomyces
 <400> 30

55
 Pro Ala Asp Gly Tyr Gln Thr Ala Lys Glu Leu Ile Arg Arg Gly His
 1 5 10 15

Arg Val Ala Ile Val Asp Ile Asp Glu Ala Arg Ala Lys Gly Ala Ala
 20 25 30

5 Ala Glu Leu Gly Val Lys Val Val Thr Arg Leu Asp Val Thr Glu Pro
 35 40 45

10 Asp Ser Phe Thr Thr Phe Leu Asp Leu Val Glu Arg Glu Leu Gly Pro
 50 55 60

15 Leu Asp Ile Leu Val Asn Asn Ala
 65 70

<210> 31

20 <211> 67

<212> PRT

<213> unknown

25 <220>

<221> source

<223> ZF0050310= *Arthrobacter paraffineus*

30 <400> 31

Ala Thr Asp Gly Ala Arg Val Ala Val Val Asp Leu His Ile Glu Ser
 1 5 10 15

35 Ala Glu Glu Thr Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala
 20 25 30

40 Leu Ala Leu Glu Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala
 35 40 45

45 Phe Glu Ala Thr Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn
 50 55 60

50 Asn Ala Gly
 65

<210> 32

<211> 67

55 <212> PRT

<213> unknown

<220>
 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 5 <400> 32
 Ala Ala Asp Gly Ala Arg Val Ala Val Val Asp Leu His Ile Glu Ser
 1 5 10 15
 Ala Lys Glu Thr Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala
 20 25 30
 15 Leu Ala Leu Glu Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala
 35 40 45
 Phe Glu Ala Thr Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn
 50 55 60
 20 Asn Ala Gly
 65
 25 <210> 33
 <211> 348
 30 <212> PRT
 <213> unknown
 <220>
 35 <221> source
 <223> ZF0050310= *Arthrobacter paraffineus*
 <400> 33
 40 Met Lys Ala Ile Gln Tyr Ala Arg Ile Gly Ala Glu Pro Glu Leu Thr
 1 5 10 15
 45 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
 20 25 30
 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
 50 35 40 45
 Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
 50 55 60
 55 Ala Gly Arg Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
 65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Ser Cys Trp
 85 90 95

5 His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Lys Glu Leu
 100 105 110

10 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

15 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 130 135 140

20 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ala Tyr Ala Val
 165 170 175

25 Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

30 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

35 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220

40 Lys Asp Ala Ala Glu Asn Val Arg Arg Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

45 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270

50 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

55 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ala Val Glu Thr
 305 310 315 320

	Phe	Ser	Leu	Asp	Asn	Gly	Ala	Glu	Ala	Tyr	Arg	Arg	Leu	Ala	Ala	Gly	
					325					330						335	
5																	
	Thr	Leu	Ser	Gly	Arg	Ala	Val	Val	Val	Pro	Gly	Leu					
				340					345								
10																	
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	<213>		unknown														
	<220>																
20																	
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	<223>		ZF0050310=														
	<400>		34														
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	1				5					10					15		
	Glu	Ile	Pro	Lys	Pro	Glu	Pro	Gly	Pro	Gly	Glu	Val	Leu	Leu	Glu	Val	
30				20					25					30			
	Thr	Ala	Ala	Gly	Val	Cys	His	Ser	Asp	Asp	Phe	Ile	Met	Ser	Leu	Pro	
35			35					40					45				
	Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly	
	50						55					60					
40																	
	Ala	Gly	Arg	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile	
	65					70					75					80	
45	Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Ser	Cys	Trp	
					85					90					95		
	His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Lys	Glu	Leu	
50				100					105					110			

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

5 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 130 135 140

10 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

15 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ala Tyr Ala Val
 165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

20 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

25 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220

30 Lys Asp Ala Ala Glu Asn Val Arg Arg Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

35 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270

40 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

45 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

50 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ala Val Glu Thr
 305 310 315 320

55 Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly
 325 330 335

Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu
 340 345

<210> 35
 <211> 488
 5 <212> DNA
 <213> unknown
 10 <220>
 <221> source
 <223> ZF0002326= *Actinoplanes missouriensis*; ZF0003505= *Streptomyces*;
 15 ZF0050197= *Pseudomonas oleovorans*; ZF0050294= *Rhodococcus*;
 ZF0050330= *Bacillus*; ZF0051303= *Bacterium*; ZF0051337=
Methylobacter; ZF0051321= *Bacterium*; ZF0050782= *Lactobacillus*
bulgaricus; ZF0050544= *Phyllobacterium rubiacearum*; ZF0002852=
Rhodococcus; ZF0050310= *Arthrobacter paraffineus*; ZF0002862=
Streptomyces clavuligerus; ZF0050292= *Bacterium*; ZF0002031=
 20 *Streptomyces*; ZF0002349= *Streptomyces spectabilis*; ZF0002434=
Streptomyces; ZF0002437= *Streptomyces*; ZF0003712=
Micromonospora; ZF0003765= *Streptomyces*; ZF0051305= *Bacterium*;
 ZF0003513= *Actinomyces*; ZF0050993= *Kocuria*; ZF0002018=
Streptomyces; ZF0003767= *Actinomyces*; ZF0002332= *Streptomyces*
 25 *diastatochromogenes*; ZF0003768= *Actinomyces*; ZF0002379=
Streptomyces coelestis; ZF0002351= *Nonomuraea roseoviolacea*;
 ZF0003769= *Actinomyces*;
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 30 gggccatggg gttgtggcaa ctgttggcac tgctcacaag gactcgagaa ctattgctct
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 cgcgcccaag aactcggaat caatcctccc ggtctcggtg caccgggccc gttggccgag
 120
 35 ttcatgatcg tcgattctcc tcgccacett gtcccgatcg gtgacctga cccggtcaag
 180
 acggtgccgc tgaccgacgc cggctctgacg ccgtatcacg cgatcaagcg ttctctgccg
 40 240
 aaacttcgcg gaggtctgta cgcggttgctc attggtaccg gcgggctcgg ccacgtcgcc
 300
 45 attcagctcc tccgtcacct ctggcgctca acggtcatcg ctttggacgt gagcgccgac
 360
 aagctcgaac tggcaaccaa ggtaggcgct cacgaagtgg ttctgtccga caaggacgag
 420
 50 gccgagaacg tccgcaagat cactggaagt caaggcgccg cactgggttct cgacttcggt
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 55 488
 <210> 36

<211> 385
<212> DNA
5 <213> unknown
<220>
<221> source
10 <223> ZF0002326= Actinoplanes missouriensis; ZF0003505= Streptomyces;
ZF0050197= Pseudomonas oleovorans; ZF0050294= Rhodococcus;
ZF0050330= Bacillus; ZF0051303= Bacterium; ZF0051337=
Methylobacter; ZF0051321= Bacterium; ZF0050782= Lactobacillus
15 bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=
Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=
Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0002031=
Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
Streptomyces; ZF0002437= Streptomyces; ZF0003712=
20 Micromonospora; ZF0003765= Streptomyces; ZF0051305= Bacterium;
ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018=
Streptomyces; ZF0003767= Actinomyces; ZF0002332= Streptomyces
diastatochromogenes; ZF0003768= Actinomyces; ZF0002379=
Streptomyces coelestis; ZF0002351= Nonomuraea roseoviolacea;
ZF0003769= Actinomyces;
25 <400> 36
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cgcgcccaag aactcggaat caatcctccc ggtctcgggtg caccgcggcgc gttggccgag
30 120
ttcatgatcg tcgattctcc tcgccacctt gtcccgatcg gtgacctcga cccggtcaag
180
35 acggtgcccgc tgaccgacgc cggctctgacg ccgtatcacg cgatcaagcg ttctctgccg
240
aaacttcgcg gaggctcgta cgcggttgtc attggtaccg gcgggctcgg ccacgtcacc
300
40 attcagctcc tccgtcacct ctccggcgga acggtcatcg ctttggacgt gagcgcgga
360
aagctcgaac tggcaaccaa ggtag
45 385
<210> 37
50 <211> 486
<212> DNA
<213> unknown
55 <220>
<221> source
<223> ZF0050286= Corynebacterium hoagii

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60
5 cgcgcaaggg aactcggcat cgccccaccc ggcttgggcg cgccggggcg gatcgccgag
120
tacatgatcg tcgactcgcc gcgtcacctg gtcccgatcg gtgacctga ccccgtcacg
10 180
acggtgccgc tgaccgacgc cgggctcacc cgtaccacg cgatcaaacg gtcgctcggc
240
15 aagctccgcg ccggctcgta cgcagtcgtg atcggcaccg gaggcctcgg acacgtcggc
300
atccagctgc tccgccacct gtcccctgca cgcattcatg ccctcgacgt caacgacgag
20 360
aagctcgcgt tcgcccgcga ggtcgggcgc caccgagaccg tgttgtcgaa cgccgacgcc
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25 gccgcgaacg tccggaagat caccgggttcg gccggtgccg cgctgggtcct agacttcgtc
480
ggctac
486
30
<210> 38
<211> 483
35 <212> DNA
<213> unknown
<220>
40
<221> source
<223> ZF0050310= *Arthrobacter paraffineus*
<400> 38
45 ggcccatggg gctgtggcag ctgttggcac tgctcgcaag gactcgaaaa ctactgttct
60
cgggcaaaa g aactcggcat caatcctcct ggtctcggtg caccgggcgc gttggccgaa
50 120
ttcatgatcg tcgattcacc tcgccacctc gtcccgatcg gcgacctga tccgggtcaag
180
acggtgccac tgaccgacgc cgggtctgact ccgtatcacg cgatcaagcg ttactgccc
55 240
aaacttcgcg gtggcgcgta cgccgtcgtc atcggtaccg gcggtctcgg ccatgtcgcc
300

atccaactcc tccgccacct ctccggcagca accgtcatcg cactcgacgt gagcgcgagc
 360
 5 aagctcgtac tggcaaccaa ggtaggcgct cacgaagtgg tcctgtccga caaggacgcg
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 gccgagaacg tccgcaggat caccggaagt cagggcgccg cactggttct tgacttcgtt
 480
 10 ggc
 483
 <210> 39
 15 <211> 210
 <212> DNA
 20 <213> unknown
 <220>
 <221> source
 25 <223> ZF0004210= Actinomyces; ZF0004212= Actinomyces; ZF0004211=
 Actinomyces; ZF0003860= Actinomyces; ZF0004218= Actinomyces;
 ZF0003868= Actinomadura; ZF0004213= Actinomyces; ZF0003876=
 Actinomyces; ZF0003866= Actinomyces; ZF0003864= Actinomyces;
 30 ZF0003862= Actinomadura; ZF0003869= Actinomyces; ZF0003867=
 Actinomadura; ZF0004216= Actinomyces; ZF0004235= Actinomyces;
 ZF0004209= Actinomadura; ZF0004214= Actinomyces; ZF0003871=
 Actinomyces; ZF0004063= Actinomadura; ZF0004052= Actinomadura;
 ZF0006405= Streptomyces; ZF0003865= Actinomadura; ZF0004047=
 Actinomadura; ZF0004070= Actinomyces; ZF0004085= Actinomyces;
 35 ZF0004217= Actinomyces; ZF0004089= Actinomadura; ZF0004090=
 Actinomadura; ZF0006138= Streptomyces; ZF0004236= Actinomadura;
 ZF0051203= Bacterium;
 <400> 39
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 cgcgccaagg aactcggcat cgccccgccc ggactcgggt cgcccggcgc catggccgag
 120
 45 tacatgatcg tcgacgaccc gcgccacctg gtgccgctcg gcggtctcga cccgggtccag
 180
 gccgtgccgc tcactgacgc gggcctgaca
 50 210
 <210> 40
 55 <211> 282
 <212> DNA
 <213> unknown

<220>

<221> source

5 <223> ZF0002326= Actinoplanes missouriensis; ZF0003505= Streptomyces;
ZF0051321= Bacterium; ZF0050782= Lactobacillus bulgaricus;
ZF0050544= Phyllobacterium rubiacearum; ZF0002031=
Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
10 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
Actinoplanes philippinensis; ZF0002441= Streptomyces;
ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
Micromonospora; ZF0004980= Streptomyces; ZF0004821=
15 Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396=
Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces;
ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087=
Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium;
ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538=
20 Actinomyces; ZF0003535= Actinomyces;

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25 ggcggggcacg aggggttcggg cgtcatacacc aagctcggcc ctgaggtcaa gggactggag
120
gtcggcgacc acgtcggttct gtccttcatt cgggcttggt gaacctgtcc ggcgtgttcg
30 180
gccggggcatc agaatctttg tgacctcggg atgggcctcc tcagcggcca agccatcagc
240
35 gacgggcacgt accggatcca ggctcgcggc gaaaacgtga tc
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<210> 41

40 <211> 276

<212> DNA

45 <213> unknown

<220>

<221> source

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ZF0050544= Phyllobacterium rubiacearum; ZF0002031=
Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
55 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
Actinoplanes philippinensis; ZF0002441= Streptomyces;
ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
Micromonospora; ZF0004980= Streptomyces; ZF0004821=

Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087= Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium; ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538= Actinomyces; ZF0003535= Actinomyces;

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<400> 41
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 10 60

ggccacgaag gcgcgggcat agtggagaaa gtcggccccg gcgtgcgaga cgtcgaggta
 120

15 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180

ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg
 240

20 acgtaccgcg cgacagctcg cgggcacgac gtcgga
 276

<210> 42

25 <211> 276

<212> DNA

<213> unknown

30 <220>

<221> source

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 ZF0050544= Phyllobacterium rubiacearum; ZF0002031= Streptomyces;
 ZF0002349= Streptomyces spectabilis; ZF0002434= Streptomyces;
 ZF0050993= Kocuria; ZF0002018= Streptomyces;
 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331= Actinoplanes philippinensis; ZF0002441= Streptomyces;
 40 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240= Bacterium;
 ZF0002333= Rhodococcus erythropolis; ZF0003713= Micromonospora;
 ZF0004980= Streptomyces; ZF0004821= Actinomyces;
 45 ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes;
 ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces;
 ZF0006103= Streptomyces; ZF0006087= Streptomyces;
 ZF0050446= Bacterium; ZF0050445= Bacterium; ZF0006086= Streptomyces;
 ZF0002322= Rhodococcus; ZF0003538= Actinomyces;
 50 ZF0003535= Actinomyces;

<400> 42
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55 ggccacgaag gcgcgggcat agtggagaaa gtcggccccg gcgtgcgaga cgtcgaggta
 120

ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180

ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg
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5 acgtaccgcg cgacagctcg cgggcacgac gtcgga
 276

10 <210> 43
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 ZF0051321= Bacterium; ZF0050782= Lactobacillus bulgaricus;
 ZF0050544= Phyllobacterium rubiacearum; ZF0002031=
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=
 Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;
 25 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=
 Actinoplanes philippinensis; ZF0002441= Streptomyces;
 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=
 Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=
 Micromonospora; ZF0004980= Streptomyces; ZF0004821=
 30 Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396=
 Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces;
 ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087=
 Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium;
 35 ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538=
 Actinomyces; ZF0003535= Actinomyces;

<400> 43
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 120

45 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180

ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg
 240

50 acgtaccgcg cgacagctcg cgggcacgac gtcgga
 276

55 <210> 44
 <211> 276
 <212> DNA

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<220>

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ZF0050544= *Phyllobacterium rubiacearum*; ZF0002031=
Streptomyces; ZF0002349= *Streptomyces spectabilis*; ZF0002434=
Streptomyces; ZF0050993= *Kocuria*; ZF0002018= *Streptomyces*;
10 ZF0003767= *Actinomyces*; ZF0003764= *Streptomyces*; ZF0002331=
Actinoplanes philippinensis; ZF0002441= *Streptomyces*;
ZF0051307= *Bacterium*; ZF0051301= *Bacterium*; ZF0051240=
Bacterium; ZF0002333= *Rhodococcus erythropolis*; ZF0003713=
Micromonospora; ZF0004980= *Streptomyces*; ZF0004821=
15 Actinomyces; ZF0002359= *Actinoplanes ianthinogenes*; ZF0002396=
Actinoplanes; ZF0003781= *Actinomyces*; ZF0003512= *Actinomyces*;
ZF0006093= *Streptomyces*; ZF0006103= *Streptomyces*; ZF0006087=
Streptomyces; ZF0050446= *Bacterium*; ZF0050445= *Bacterium*;
ZF0006086= *Streptomyces*; ZF0002322= *Rhodococcus*; ZF0003538=
20 Actinomyces; ZF0003535= *Actinomyces*;

<400> 44
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30 180
ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacag ggtcgacggg
240
35 acgtaccgcg cgacagctcg cgggcacgac gtcgga
276

<210> 45

40 <211> 276

<212> DNA

45 <213> unknown

<220>

<221> source

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ZF0051321= *Bacterium*; ZF0050782= *Lactobacillus bulgaricus*;
ZF0050544= *Phyllobacterium rubiacearum*; ZF0002031=
Streptomyces; ZF0002349= *Streptomyces spectabilis*; ZF0002434=
Streptomyces; ZF0050993= *Kocuria*; ZF0002018= *Streptomyces*;
55 ZF0003767= *Actinomyces*; ZF0003764= *Streptomyces*; ZF0002331=
Actinoplanes philippinensis; ZF0002441= *Streptomyces*;
ZF0051307= *Bacterium*; ZF0051301= *Bacterium*; ZF0051240=
Bacterium; ZF0002333= *Rhodococcus erythropolis*; ZF0003713=
Micromonospora; ZF0004980= *Streptomyces*; ZF0004821=

Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087= Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium; ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538= Actinomyces; ZF0003535= Actinomyces;

5

<400> 45
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 60
 ggccacgaag gcgcgggcat agtggagaaa gtcggccccc gcgtgcgaga cgtcgaggta
 120
 15 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc
 180
 ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg
 240
 20 acgtaaccgcg cgacagctcg cgggcacgac gtcgga
 276
 <210> 46
 25 <211> 279
 <212> .DNA
 <213> unknown
 30 <220>
 <221> source
 <223> ZF0050310= Arthrobacter paraffineus
 35
 <400> 46
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 40 gggcacgaag gagcgggggt ggtcgaggcc gtcggctcgt cgatcgacag cattgcgccc
 120
 ggtgatcacg tgttgctgag ctaccgcagt tcgggtgtgt gcaggcagtg cctcagcggg
 180
 45 catcgggctg actgcgaaag ctcacacggg ctcaacagct ctggcgacag caccgacggc
 240
 tcgacgccgg tccggcgaag cggaactccg atacggtcc
 50 279
 <210> 47
 55 <211> 279
 <212> DNA
 <213> unknown

<220>
 <221> source
 5 <223> ZF0002333= Rhodococcus erythropolis
 <400> 47
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 10 ggacacgaag ggcgcggcgt cgtgcaagcc gttggctcgt cgatcgacaa catcgcggt
 120
 15 ggtgatcacg tattgctgag ctaccgcagt tgcggtgtat gcaggcaatg tctcagcgac
 180
 catcggggcgt actgcgaaaag ctcacacggg ctcaacagct ctggcgcacg caccgacggc
 240
 20 tgcagcgccgg tccggcgaaa cggaactccg atacgggtcc
 279
 <210> 48
 25 <211> 360
 <212> DNA
 <213> unknown
 30 <220>
 <221> source
 35 <223> ZF0051303= Bacterium; ZF0051337= Methylomonas; ZF0002862=
 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0051305=
 Bacterium; ZF0003513= Actinomyces; ZF0002351= Nonomuraea
 roseoviolacea; ZF0003769= Actinomyces; ZF0002017= Streptomyces;
 40 ZF0051306= Bacterium; ZF0002016= Streptomyces; ZF0003504=
 Actinomyces; ZF0006073= Streptomyces; ZF0003770= Actinomyces;
 ZF0002352= Actinoplanes italicus; ZF0002378= Streptomyces
 aureomonopodiales; ZF0006089= Streptomyces; ZF0006106=
 Streptomyces; ZF0051325= Bacterium; ZF0006108= Streptomyces;
 ZF0002440= Streptomyces; ZF0051302= Bacterium; ZF0003532=
 45 Actinomyces; ZF0003548= Nocardiaform;
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 50 cacctcgtcc tcgggcacga atcgctgggc cgagtacgca ccgcgcccga cggcagcgg
 120
 ttgcgcgccg gtgatctcgt cgtcgggata gtgcgcaggc ccgatccggt gccgtgcggg
 180
 55 gcgtgtgcgc acggtgagtt cgacatgtgc cgcaacggtg agtacgtcga gcgcgggata
 240

aagcagatcg acgggtacgg gtcgacgtcg tgggtggtgg acgccgacta cacggtcaag
 300
 ctggaccg cgctcaccga ggtgggtgtg ctgatggaac cgacgacggt gcttggccaa
 5 360
 <210> 49
 10 <211> 421
 <212> DNA
 <213> unknown
 15 <220>
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 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0051305=
 Bacterium; ZF0003513= Actinomyces; ZF0002351= Nonomuraea
 roseoviolacea; ZF0003769= Actinomyces; ZF0002017= Streptomyces;
 ZF0051306= Bacterium; ZF0002016= Streptomyces; ZF0003504=
 Actinomyces; ZF0006073= Streptomyces; ZF0003770= Actinomyces;
 25 ZF0002352= Actinoplanes italicus; ZF0002378= Streptomyces
 aureomonopodiales; ZF0006089= Streptomyces; ZF0006106=
 Streptomyces; ZF0051325= Bacterium; ZF0006108= Streptomyces;
 ZF0002440= Streptomyces; ZF0051302= Bacterium; ZF0003532=
 Actinomyces; ZF0003548= Nocardiaform;
 30 <400> 49
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 60
 35 ccgctcacgc tcggccacga gttcgtcggc gaggtcgtcg agaccggccg cgacgtgacc
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 gacatccagg tcggcgacct ggtcagcggc gagggccacc tgggtctgagg caagtgccgc
 180
 40 aactgcctgg ccggccgccc tcacctgtgc cgcgcgaccg tcggcctcgg tgtcggccgt
 240
 45 gacggcgcct tcgccagata cgtggtgctg cccgcctcca acgtgtgggt gcaccgggtg
 300
 ccggtcgacc tcgacgtcgc cgcgatcttc gaccggttcg gcaacgagggt gcacaccgag
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 50 ctctccttcc cgctcgtcgg cgaggacgtg ctggtcaccg gtgccgggtac catcggcac
 420
 t
 421
 55 <210> 50
 <211> 414

<212> DNA
 <213> unknown
 5 <220>
 <221> source
 10 <223> ZF0050197= *Pseudomonas oleovorans*; ZF0050294= *Rhodococcus*;
 ZF0050330= *Bacillus*, ZF0002852= *Rhodococcus*; ZF0050310=
Arthrobacter paraffineus; ZF0002437= *Streptomyces*; ZF0003712=
Micromonospora; ZF0003765= *Streptomyces*; ZF0002332=
 15 *Streptomyces diatsatochromogenes*; ZF0003768= *Actinomyces*;
 ZF0002379= *Streptomyces coelestis*; ZF0002443= *Streptomyces*;
 ZF0002442= *Streptomyces*; ZF0002436= *Streptomyces*; ZF0050994=
Bacterium; ZF0050992= *Bacterium*; ZF0050442= *Bacterium*;
 ZF0002049= *Streptomyces*; ZF0006069= *Streptomyces*; ZF0006075=
Streptomyces; ZF0004724= *Nocardiaform*; ZF0002392= *Actinoplanes*
 20 *nipponensis*; ZF0002356= *Actinoplanes brasiliensis*; ZF0003501=
Actinomyces; ZF0051322= *Bacterium*; ZF0006078= *Streptomyces*;
 ZF0006092= *Streptomyces*; ZF0006090= *Streptomyces*; ZF0006084=
Streptomyces; ZF0006068= *Streptomyces*; ZF0050284= *Rhodococcus*;
 ZF0050028= *Agrobacterium tumefaciens*; ZF0003540= *Actinomyces*;
 25 ZF0003528= *Actinomyces*; ZF0003529= *Actinomyces*;
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 30 ggttaccgag agggccaacg cgtgatcgcc ggccgcatct gcccgaactt caattcgat
 120
 gccgcgcagg atggcgcgcc gtcgcaggat ggcagctacc tggcggccag cggcgcatgc
 180
 35 ggctgccatg gataccgggc caccggcggc tggcgctttg gcaacatcat cgatggcgcc
 240
 caggccgaat acctgctggt tcccgatgag caggcgcaatc tggcgccggt tccggacaac
 40 300
 ctgagcgatg aacagggtgct gatgtgcccg gacatcatgt ccaccggctt caaaggcgca
 360
 45 gagaacgcac acatccgcat cggcgacacg gtggcggtat ttgcgcaggg acca
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 <210> 51
 50 <211> 432
 <212> DNA
 55 <213> unknown
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Arthrobacter paraffineus; ZF0002437= *Streptomyces*; ZF0003712=
Micromonospora; ZF0003765= *Streptomyces*; ZF0002332=
 5 *Streptomyces diatsatochromogenes*; ZF0003768= *Actinomyces*;
 ZF0002379= *Streptomyces coelestis*; ZF0002443= *Streptomyces*;
 ZF0002442= *Streptomyces*; ZF0002436= *Streptomyces*; ZF0050994=
Bacterium; ZF0050992= *Bacterium*; ZF0050442= *Bacterium*;
 10 ZF0002049= *Streptomyces*; ZF0006069= *Streptomyces*; ZF0006075=
Streptomyces; ZF0004724= *Nocardiaform*; ZF0002392= *Actinoplanes*
nipponensis; ZF0002356= *Actinoplanes brasiliensis*; ZF0003501=
Actinomyces; ZF0051322= *Bacterium*; ZF0006078= *Streptomyces*;
 ZF0006092= *Streptomyces*; ZF0006090= *Streptomyces*; ZF0006084=
Streptomyces; ZF0006068= *Streptomyces*; ZF0050284= *Rhodococcus*;
 15 ZF0050028= *Agrobacterium tumefaciens*; ZF0003540= *Actinomyces*;
 ZF0003528= *Actinomyces*; ZF0003529= *Actinomyces*;

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 120
 25 ccggggcgatc gcgtgctcgt ctcgtgtgtc accgcatgcg gtacgtgccg gttctgccgc
 180
 gagagccgct acgggcaatg cctcggaggc ggcggctgga tcctcggaca cctgatcgac
 240
 30 ggcacccagg ccgaactcgt ccgagttccg tacgccgaca attcgaccca ccgcatcccc
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 gacgggtgtga gcgacgagca gatgctcatg ctcgccgaca tcctgcccac ctctacgag
 35 360
 gtcgggtgttc tcaacggctg tctccggccg gcggacgtcg tcgtcatcat cggggccgac
 420
 40 gatcggcctc tt
 432

45 <210> 52

<211> 220

<212> DNA

50 <213> unknown

<220>

<221> source

55 <223> ZF0050310= *Arthrobacter paraffineus*

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 60

tcacgagcgc gtcacgtccg agattcagct caacatcgcc acgctggtcg agctgacaca
120

5 cacattcccg cccgaccttc tcaccggccg cggagcactg gtcaacatcg ccagcacaga
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gtcgttccag cccgacaccg gcatggccgt ctactgcgct
220

10

<210> 53

<211> 226

15 <212> DNA

<213> unknown

20 <220>

<221> source
<223> ZF0050310= *Arthrobacter paraffineus*

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60

tctcgagcgc gtcacgtccg agattcagct caacatcgcc acgctggtcg agctgacaca
120

30 cacattcctg cccgaccttc tcaccggccg cggagcactg gtcaacatcg ccagcacaga
180

35 gtcgttccag cccgacaccg gcatggccgt ctactgcgcc accaag
226

<210> 54

40 <211> 237

<212> DNA

45 <213> unknown

<220>

<221> source
50 <223> ZF0003535= *Actinomyces*

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60

55 acccccgcgc attttgagcg catcctgcgg gtgaacctga ccggcgtctt caacctgagc
120

caagccgtca ttcccttgat gattcagcgc ggccggaggaa gcatcgcttc gatttcctcg
180

5 ctgtcggcgc agaacggcgg ggggatcttc ggccggcgccc actattgcgc aaccaag
237

<210> 55

10 <211> 229

<212> DNA

<213> unknown

15 <220>

<221> source

20 <223> ZF0003535= Actinomyces

<400> 55
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25 gccgctaaag gactggcaga ccatggtgaa caccaacatc accggtctac tgaacatcac
120

ccaccatctc ctgccgacac tgatcgaccg taaaggatc gtcgtcaacc ttctgtctgt
180

30 tgccgcgcac tatccctata cgggcggcaa tgtatactgc gcctccaag
229

35 <210> 56

<211> 216

<212> DNA

40 <213> unknown

<220>

45 <221> source

<223> ZF0050310= Arthrobacter paraffineus

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50 60

ggcgacatcg acgaagccac tctcgcgcga gcagccaagg atttgggcat ccgcacgttc
120

55 gggcgccctcg acgtcaccga cccgcctcg ttcttcgact tcctcgacac cgtcgaaggt
180

gaactcggcc cgatcgacgt gctgatcaac aacgcg
216

<210> 57

5 <211> 225

<212> DNA

<213> unknown

10 <220>

<221> source

<223> ZF0080310= *Arthrobacter paraffineus*

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120

gcccggtttcg cttcctgcga cgtgcgtgac tccggacagg tcgaggccat gctcgatctg
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<210> 58

30 <211> 216

<212> DNA

35 <213> unknown

<220>

<221> source

40 <223> ZF0080310= *Arthrobacter paraffineus*

<400> 58

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120

50 acccgctctg atgtcaccga ccctgactcg ttcaaagact ttctcgacct agtcgagggga
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gacctcggcc ccctcgacgt gctgatcaac aacgcg
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55 <210> 59

<211> 222

<212> DNA

<213> unknown

5 <220>

<221> source

<223> ZF0080310= *Arthrobacter paraffineus*

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120

cgtttcgcctt cctgcgacgt gcgtgactcc ggacaggctc aggccatgct cgatctggcc
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<211> 222

25 <212> DNA

<213> unknown

30 <220>

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40 atcaacgaaa ccgtgggaac ggctgcggtc ggcgaactcg gtggagagtc ggtcgcccgt
120

ttcgcttcct gcgacgtgcg tgactccgga caggctcagg ccatgctcga tctggccgaa
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<221> source

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186
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40 222
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120

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15 <212> DNA

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20 <221> source

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120

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180

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216

35 <210> 65

40 <211> 201

<212> DNA

<213> unknown

45 <220>

<221> source

50 <223> ZF0050310= Arthrobacter paraffineus

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gaccgcgccg ccgtgagcgc cgctttcgaa gccaccgtcg ccgaatgggg acgcttcgac
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 120

 gacgacttca tcatgagcct gcccgagag cagtacacct acggccttcc tctcacgctc
180

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 540
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 720
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gacgacttca tcatgagcct gccgaagag cagtacacct acggccttcc tctcacgctc
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gcacccggcg cgttggccga attcatgata gtcgattcac ctcgccacct cgtcccgata
420

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600

25 gcactcgacg tgagcgcgga caagctcgaa ctggcaacca aggtaggcgc tcacgaagtg
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720

30 gcactgggttc tcgacttcgt cggctatcag ccaccatcg acaccgcgat ggctgtcgcc
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ggcgtcggat cggacgtcac gatcgtcggg atcggcgacg ggcaggccca tgccaaagtc
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900

40 gagctgatcg aattgatcga cctggcgcac gccggcatct tcgacatcg ggtggagacc
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1020

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